

SEQUENCE LISTING

<110> Moore, K.
 Nagle, D.
 Woolf, E.

<120> NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR

<130> 7853-119

<140> 09/062,753
 <141> 1998-04-17

<150> 08/833,226
 <151> 1997-04-17

<160> 8

<170> FastSEQ for Windows Version 3.0

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 <222> (45) . . . (1196)

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 Asn Gly Asn Thr Ser Phe Thr Pro Asn Phe Asn Pro Pro Gln Asp His
 5 10 15 20

gcc tcc tcc ctc tcc ttt aac ttc agt tat ggt gat tat gac ctc cct 152
 Ala Ser Ser Leu Ser Phe Asn Phe Ser Tyr Gly Asp Tyr Asp Leu Pro
 25 30 35

atg gat gag gat gag gac atg acc aag acc cgg acc ttc ttc gca gcc 200
 Met Asp Glu Asp Glu Asp Met Thr Lys Thr Arg Thr Phe Phe Ala Ala
 40 45 50

aag atc gtc att ggc att gca ctg gca ggc atc atg ctg gtc tgc ggc 248
 Lys Ile Val Ile Gly Ile Ala Leu Ala Gly Ile Met Leu Val Cys Gly
 55 60 65

atc ggt aac ttt gtc ttt atc gct gcc ctc acc cgc tat aag aag ttg 296
 Ile Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg Tyr Lys Lys Leu
 70 75 80

2

cgc aac ctc acc aat ctg ctc att gcc aac ctg gcc atc tcc gac ttc Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe 85 90 95 100	344
ctg gtg gcc atc atc tgc tgc ccc ttc gag atg gac tac tac gtg gta Leu Val Ala Ile Ile Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val 105 110 115	392
cgg cag ctc tcc tgg gag cat ggc cac gtg ctc tgt gcc tcc gtc aac Arg Gln Leu Ser Trp Glu His Gly His Val Leu Cys Ala Ser Val Asn 120 125 130	440
tac ctg cgc acc gtc tcc ctc tac gtc tcc acc aat gcc ttg ctg gcc Tyr Leu Arg Thr Val Ser Leu Tyr Val Ser Thr Asn Ala Leu Leu Ala 135 140 145	488
att gcc att gac aga tat ctc gcc atc gtt cac ccc ttg aaa cca cgg Ile Ala Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Lys Pro Arg 150 155 160	536
atg aat tat caa acg gcc tcc ttc ctg atc gcc ttg gtc tgg atg gtg Met Asn Tyr Gln Thr Ala Ser Phe Leu Ile Ala Leu Val Trp Met Val 165 170 175 180	584
tcc att ctc att gcc atc cca tcg gct tac ttt gca aca gaa acc gtc Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe Ala Thr Glu Thr Val 185 190 195	632
ctc ttt att gtc aag agc cag gag aag atc ttc tgt ggc cag atc tgg Leu Phe Ile Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp 200 205 210	680
cct gtg gat cag cag ctc tac tac aag tcc tac ttc ctc atc ttt Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe 215 220 225	728
ggt gtc gag ttc gtg ggc cct gtg gtc acc atg acc ctc tgc tat gcc Gly Val Glu Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala 230 235 240	776
agg atc tcc cgg gag ctc tgg ttc aag gca gtc cct ggg ttc cag acg Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr 245 250 255 260	824
gag cag att cgc aag cgg ctg cgc tgc cgc agg aag acg gtc ctg gtg Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val 265 270 275	872
ctc atg tgc att ctc acg gcc tat gtg ctg tgc tgg gca ccc ttc tac Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr 280 285 290	920
ggt ttc acc atc gtt cgt gac ttc ttc ccc act gtg ttc gtg aag gaa Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu 295 300 305	968

ccagctcctc	aggaggctga	ggcatgagaa	ttgcttgaac	cccagaggca	gagggtgcag	3546
tgaattgaga	tcgcaccact	gcactccagc	ctgggtgata	gagcaagatt	ccatctcaa	3606
aggaaaataa	aagaaaatgc	aaacacacta	taatattagc	ctaagcaaaa	ctgttaattc	3666
tgatattaca	aaattcttac	ttgcttggct	ttgaaatgca	ttgtgtata	atgcatttca	3726
aagccaagca	agtaacaatt	tttaggttatg	tacatttcta	taaatataat	aattgtattt	3786
ttattttata	ttctatcctg	gctcttagcc	gaatcaggag	attctttagg	aatggaccat	3846
gtaccagtca	agtctgtcag	caggattcat	caccctgttc	cttttgtcc	tagaatatac	3906
caacttcctt	tcattgaaat	ttaactgaaa	aaactttgt	aaatatcagt	gtgtatttgt	3966
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aaaaaaaaaa	aaaaaagggc	ggccgc				4052

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 <213> Homo sapiens

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20	25	30				
Tyr Asp Leu Pro Met Asp Glu Asp Glu Asp Met Thr Lys Thr Arg Thr						
35	40	45				
Phe Phe Ala Ala Lys Ile Val Ile Gly Ile Ala Leu Ala Gly Ile Met						
50	55	60				
Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg						
65	70	75	80			
Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala						
85	90	95				
Ile Ser Asp Phe Leu Val Ala Ile Ile Cys Cys Pro Phe Glu Met Asp						
100	105	110				
Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His Val Leu Cys						
115	120	125				
Ala Ser Val Asn Tyr Leu Arg Thr Val Ser Leu Tyr Val Ser Thr Asn						
130	135	140				
Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu Ala Ile Val His Pro						
145	150	155	160			
Leu Lys Pro Arg Met Asn Tyr Gln Thr Ala Ser Phe Leu Ile Ala Leu						
165	170	175				
Val Trp Met Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe Ala						
180	185	190				
Thr Glu Thr Val Leu Phe Ile Val Lys Ser Gln Glu Lys Ile Phe Cys						
195	200	205				
Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe						
210	215	220				
Leu Phe Ile Phe Gly Val Glu Phe Val Gly Pro Val Val Thr Met Thr						
225	230	235	240			
Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val Pro						
245	250	255				
Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg Lys						
260	265	270				
Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys Trp						
275	280	285				
Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr Val						
290	295	300				
Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Val Val Glu Cys		315	320			
305	310					

Ile Ala Met Ser Asn Ser Met Ile Asn Thr Val Cys Phe Val Thr Val
 325 330 335
 Lys Asn Asn Thr Met Lys Tyr Phe Lys Lys Met Met Leu Leu His Trp
 340 345 350
 Arg Pro Ser Gln Arg Gly Ser Lys Ser Ser Ala Asp Leu Asp Leu Arg
 355 360 365
 Thr Asn Gly Val Pro Thr Thr Glu Glu Val Asp Cys Ile Arg Leu Lys
 370 375 380

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 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (269) ... (1411)

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 tggAACCCG CTTTCAGAT CCTGGATGGT ATCTGTTCTC CCTAAGGATT CTAACAGGGA 180
 CCTGCACTCA CTGACCCCCAG CAGAACTGTCT GAACTCCACG TGAGCGCATC TCCCCTGATAAC 240
 ACACCAGCCC ACCTGTAGCA TCATCAAC ATG GGA CCC CAG AAC AGA AAC ACT 292
 Met Gly Pro Gln Asn Arg Asn Thr
 1 5

agc ttt gca cca gac ttg aat cca ccc caa gac cat gtc tcc tta aac 340
 Ser Phe Ala Pro Asp Leu Asn Pro Pro Gln Asp His Val Ser Leu Asn
 10 15 20

tac agt tat ggt gat tat gac ctc ccc ctg ggt gag gat gag gat gtg 388
 Tyr Ser Tyr Gly Asp Tyr Asp Leu Pro Leu Gly Glu Asp Glu Asp Val
 25 30 35 40

acc aag aca cag acc ttc ttt gca gcc aaa att gtc att ggc gtg gca 436
 Thr Lys Thr Gln Thr Phe Phe Ala Ala Lys Ile Val Ile Gly Val Ala
 45 50 55

ctg gca ggc atc atg ctg gtc tgc ggc att ggc aac ttt gtc ttc att 484
 Leu Ala Gly Ile Met Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile
 60 65 70

gct gcc ctc gcc cgc tac aag aag ctg cgc aac ctt acc aac ctc ctc 532
 Ala Ala Leu Ala Arg Tyr Lys Leu Arg Asn Leu Thr Asn Leu Leu
 75 80 85

att gct aac ctg gcc atc tct gac ttc ctg gtg gcg atc gtc tgc tgc 580
 Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala Ile Val Cys Cys
 90 95 100

ccc ttt gag atg gac tat tat gta gta cgg cag ctt tcc tgg gcg cat 628
 Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu Ser Trp Ala His
 105 110 115 120

ggt cac gtg ctt tgt gcc tcc gtc aac tac ctt cgt acg gtc tcc ctg 676
 Gly His Val Leu Cys Ala Ser Val Asn Tyr Leu Arg Thr Val Ser Leu
 125 130 135

One set of 25 sets/60

tac gtc tcc acc aac gct ctg ctg gcc atc gct att gac aga tac ctc Tyr Val Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu 140 145 150	724
gct att gtc cac cct ttg aaa cca cg ^g atg aat tat cag acc gct tcc Ala Ile Val His Pro Leu Lys Pro Arg Met Asn Tyr Gln Thr Ala Ser 155 160 165	772
ttc ctg atc gct ttg gtc tgg atg gtc tcc atc ctc atc gct gtc cca Phe Leu Ile Ala Leu Val Trp Met Val Ser Ile Leu Ile Ala Val Pro 170 175 180	820
tct gcc tac ttc acc aca gaa acc atc ctc gtt atc gtc aag aat caa Ser Ala Tyr Phe Thr Thr Glu Thr Ile Leu Val Ile Val Lys Asn Gln 185 190 195 200	868
gaa aaa atc ttc tgt ggt cag atc tgg tcg gtg gac cag cag ctc tac Glu Lys Ile Phe Cys Gly Gln Ile Trp Ser Val Asp Gln Gln Leu Tyr 205 210 215	916
tac aaa tcc tac ttc ctc ttc gtc ttc ggg ctt gag ttc gtg ggt ccc Tyr Lys Ser Tyr Phe Leu Phe Val Phe Gly Leu Glu Phe Val Gly Pro 220 225 230	964
gtg gtc act atg acc ctg tgc tat gcc agg atc tcc caa gag ctc tgg Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser Gln Glu Leu Trp 235 240 245	1012
ttc aag gct gta cct ggc ttc cag acg gag caa atc cgc aag cgg ctg Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu 250 255 260	1060
cgt tgc cgc cgc aag aca gtg cta ctg ctc atg ggc atc ctc aca gcc Arg Cys Arg Arg Lys Thr Val Leu Leu Met Gly Ile Leu Thr Ala 265 270 275 280	1108
tac gtg ctg tgc tgg gcg ccg ttc tat ggc ttt acc ata gtg cga gag Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp 285 290 295	1156
ttc ttc ccc acg gta gtt gtg aag gag aag cac tac ctc acc gcc ttc Phe Phe Pro Thr Val Val Val Lys Glu Lys His Tyr Leu Thr Ala Phe 300 305 310	1204
tac gtc gtg gag tgc att gcc atg agc aac agc atg atc aat act ata Tyr Val Val Glu Cys Ile Ala Met Ser Asn Ser Met Ile Asn Thr Ile 315 320 325	1252
tgc ttc gtg acg gtc aag aac aac acc atg aaa tac ttc aag aag atg Cys Phe Val Thr Val Lys Asn Asn Thr Met Lys Tyr Phe Lys Lys Met 330 335 340	1300
ctg cgg ctc cac tgg cgg ccc tct cac tac ggg agt aag tcc agc gct Leu Arg Leu His Trp Arg Pro Ser His Tyr Gly Ser Lys Ser Ser Ala 345 350 355 360	1348

200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380

Leu	Arg	Asn	Leu	Thr	Asn	Leu	Leu	Ile	Ala	Asn	Leu	Ala	Ile	Ser	Asp
85						90					95				
Phe	Leu	Val	Ala	Ile	Val	Cys	Cys	Pro	Phe	Glu	Met	Asp	Tyr	Tyr	Val
100						105					110				
Val	Arg	Gln	Leu	Ser	Trp	Ala	His	Gly	His	Val	Leu	Cys	Ala	Ser	Val
115						120					125				
Asn	Tyr	Leu	Arg	Thr	Val	Ser	Leu	Tyr	Val	Ser	Thr	Asn	Ala	Leu	Leu
130						135					140				
Ala	Ile	Ala	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro	Leu	Lys	Pro
145						150					155			160	
Arg	Met	Asn	Tyr	Gln	Thr	Ala	Ser	Phe	Leu	Ile	Ala	Leu	Val	Trp	Met
											165		170		175
Val	Ser	Ile	Leu	Ile	Ala	Val	Pro	Ser	Ala	Tyr	Phe	Thr	Thr	Glu	Thr
											180		185		190
Ile	Leu	Val	Ile	Val	Lys	Asn	Gln	Glu	Lys	Ile	Phe	Cys	Gly	Gln	Ile
											195		200		205
Trp	Ser	Val	Asp	Gln	Gln	Leu	Tyr	Tyr	Lys	Ser	Tyr	Phe	Leu	Phe	Val
											210		215		220
Phe	Gly	Leu	Glu	Phe	Val	Gly	Pro	Val	Val	Thr	Met	Thr	Leu	Cys	Tyr
											225		230		235
															240
Ala	Arg	Ile	Ser	Gln	Glu	Leu	Trp	Phe	Lys	Ala	Val	Pro	Gly	Phe	Gln
											245		250		255
Thr	Glu	Gln	Ile	Arg	Lys	Arg	Leu	Arg	Cys	Arg	Arg	Lys	Thr	Val	Leu
											260		265		270
Leu	Leu	Met	Gly	Ile	Leu	Thr	Ala	Tyr	Val	Leu	Cys	Trp	Ala	Pro	Phe
											275		280		285
Tyr	Gly	Phe	Thr	Ile	Val	Arg	Asp	Phe	Phe	Pro	Thr	Val	Val	Val	Lys
											290		295		300
Glu	Lys	His	Tyr	Leu	Thr	Ala	Phe	Tyr	Val	Val	Glu	Cys	Ile	Ala	Met
											305		310		315
Ser	Asn	Ser	Met	Ile	Asn	Thr	Ile	Cys	Phe	Val	Thr	Val	Lys	Asn	Asn
											325		330		335
Thr	Met	Lys	Tyr	Phe	Lys	Lys	Met	Leu	Arg	Leu	His	Trp	Arg	Pro	Ser
											340		345		350
His	Tyr	Gly	Ser	Lys	Ser	Ser	Ala	Asp	Leu	Asp	Leu	Lys	Thr	Ser	Gly
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Val	Pro	Ala	Thr	Glu	Glu	Val	Asp	Cys	Ile	Arg	Leu	Lys			
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<223> Primer

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<212> DNA
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<400> 6
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23

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<220>
<223> Primer

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22

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

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22